

4705



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RAW SEQUENCE LISTING

DATE: 03/01/2002

PATENT APPLICATION: US/10/076,069

TIME: 13:32:40

Input Set : A:\hepp sequence listing-US.txt

Output Set: N:\CRF3\03012002\J076069.raw

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3 <110> APPLICANT: JURECIC, ROLAND
4   NACHTMAN, RONALD
6 <120> TITLE OF INVENTION: HEPP, A NOVEL GENE WITH A ROLE IN HEMATOPOIETIC AND NEURAL
DEVELOPMENT
8 <130> FILE REFERENCE: 39532-176599
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/076,069
C--> 10 <141> CURRENT FILING DATE: 2002-02-15
10 <150> PRIOR APPLICATION NUMBER: US 60/268,923
11 <151> PRIOR FILING DATE: 2001-02-16
13 <160> NUMBER OF SEQ ID NOS: 11
15 <170> SOFTWARE: PatentIn version 3.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 2082
19 <212> TYPE: DNA
20 <213> ORGANISM: Mus musculus
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (191)..(901)
26 <400> SEQUENCE: 1
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29 gggggactgg accttcctg gcttttagca ggcgcgagcg ccatggcgac cctttgctgg      120
31 gcaggtgacc gattccgggt gccgaagga gctggcgtgg gtctgccttg cagccgcccg      180
33 cctggacagg atg ttt gct aga ggg ctg aag agg aaa tat ggt gac cag      229
34 Met Phe Ala Arg Gly Leu Lys Arg Lys Tyr Gly Asp Gln
35      1              5              10
37 gaa gaa gga gta gag ggt ttt ggc act gtc cct tcc tat agc ctg cag      277
38 Glu Glu Gly Val Glu Gly Phe Gly Thr Val Pro Ser Tyr Ser Leu Gln
39      15              20              25
41 cga cag tca ctc ctg gac atg tcc ctt gtc aag ctc cag ctc tgt cac      325
42 Arg Gln Ser Leu Leu Asp Met Ser Leu Val Lys Leu Gln Leu Cys His
43 30              35              40              45
45 atg cta gtg gag ccc aat ctc tgc cgc tcg gtc ctc atc gcc aac aca      373
46 Met Leu Val Glu Pro Asn Leu Cys Arg Ser Val Leu Ile Ala Asn Thr
47      50              55              60
49 gtc cgg cag atc cag gag gaa atg agc cag gat ggt gtg tgg cat ggg      421
50 Val Arg Gln Ile Gln Glu Glu Met Ser Gln Asp Gly Val Trp His Gly
51      65              70              75
53 atg gca ccc cag aat gta gat cgg gca cca gtt gaa cgc ctg gtg tcc      469
54 Met Ala Pro Gln Asn Val Asp Arg Ala Pro Val Glu Arg Leu Val Ser
55      80              85              90
57 aca gag atc ctg tgt cgt aca gtg agg gga gct gag gaa gag cac cct      517
58 Thr Glu Ile Leu Cys Arg Thr Val Arg Gly Ala Glu Glu Glu His Pro
59      95              100              105
61 gct cct gaa ctg gaa gat gct ccc ttg caa aac tcg gtt tcc gag ctc      565

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62 Ala Pro Glu Leu Glu Asp Ala Pro Leu Gln Asn Ser Val Ser Glu Leu
63 110 115 120 125
65 ccc atc gtt ggc tca gca cca ggg caa agg aac cct cag agc agc ctc 613
66 Pro Ile Val Gly Ser Ala Pro Gly Gln Arg Asn Pro Gln Ser Ser Leu
67 130 135 140
69 tgg gag atg gac agc cca caa gaa aac agg gga agc ttt cag aag tca 661
70 Trp Glu Met Asp Ser Pro Gln Glu Asn Arg Gly Ser Phe Gln Lys Ser
71 145 150 155
73 ctg gac cag ata ttt gag acc ctg gag aac aaa aac tcc agt tca gtg 709
74 Leu Asp Gln Ile Phe Glu Thr Leu Glu Asn Lys Asn Ser Ser Ser Val
75 160 165 170
77 gag gaa ctc ttc tca gat gtg gac agc tcc tac tat gac ctg gac aca 757
78 Glu Glu Leu Phe Ser Asp Val Asp Ser Ser Tyr Tyr Asp Leu Asp Thr
79 175 180 185
81 gtg cta aca gga atg atg agt ggg acc aag tcc agt ctc tgc aat ggc 805
82 Val Leu Thr Gly Met Met Ser Gly Thr Lys Ser Ser Leu Cys Asn Gly
83 190 195 200 205
85 ctt gag ggc ttt gct gca gcc acc cct cct ccc agt tcc act tgc aag 853
86 Leu Glu Gly Phe Ala Ala Thr Pro Pro Ser Ser Thr Cys Lys
87 210 215 220
89 tct gac ctg gct gag ctg gac cat gtg gta gag att ctg gtg gag acc 901
90 Ser Asp Leu Ala Glu Leu Asp His Val Val Glu Ile Leu Val Glu Thr
91 225 230 235
93 tgagaggcca ccccatggg ctaagggtga ggccaccagt ccccatggag ctcacgtgtg 961
95 ttgtgaccca gagacagata agcacttgct ctaagagggg ctctggctct tgagctcatt 1021
97 atccttttgt gtgacattgg actcactgtg gaggatgggtg tgtcacagct atgtctagtc 1081
99 tattttcaat tagatagggtg aactttctaa aattaagttt tatatgtttt tgggcaatat 1141
101 ttgtgtctaa gatataatttt ttaaactttt tatacttttag atttttttca gctattttct 1201
103 taaaagtata tttttctac aaacatcctc tgctgtctaca ttagaaacat ttataaccta 1261
105 aatacgattg gtgtgtcatt ttaaagggtt aaatagaaaa cttcttttgt tactgagtct 1321
107 ctacactccc aaggcaactg taaatgtagc cggccgggtg tttacatgag aggcctcact 1381
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111 gggctctgctc tggcggatcg gagctctctt cctagccccc tgtgcaggat ggctttatct 1501
113 atgcctatct atagttaa gccaactgaaa gctaagggtct tactcctgga aatcccaaca 1561
115 ccagttcttc agggactgct gtgaggcagt gccttatgca ggtcttgctc ttggccatca 1621
117 ctgtctgggt cccagcccag cacatgtgac atgaggacat gacatgcccg aaccacccag 1681
119 caccacatgc tccatgtcaa gtgtgtacgt ggagaccact ggctcccagg cctgtgctca 1741
121 gagagggtgt gcagtcctac gtgtgctggg ggggacgacg gtgacctgtg cttgcttgct 1801
123 tttaaaatgg tgcttgagcg ttttaagggtt aaaaacaatc cgactccata tgatttaggg 1861
125 ctctccacc ctggggtggc ccctatgctg tctgcttgga tctcaaagtc ttggtactcg 1921
127 gcaactgtcag actccacccc atgtatcctt ttgtttctc ttgtgctttt ttgtgacttc 1981
129 ccaacctgag cctaagggtt tattttatat gtgcttcaat atcaacaatg taaacctcac 2041
131 tttattaaaa gtatccagca aatggaaaaa aaaaaaaaaa a 2082
134 <210> SEQ ID NO: 2
135 <211> LENGTH: 237
136 <212> TYPE: PRT
137 <213> ORGANISM: Mus musculus
139 <400> SEQUENCE: 2
141 Met Phe Ala Arg Gly Leu Lys Arg Lys Tyr Gly Asp Gln Glu Glu Gly

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142 1           5           10           15
145 Val Glu Gly Phe Gly Thr Val Pro Ser Tyr Ser Leu Gln Arg Gln Ser
146           20           25           30
149 Leu Leu Asp Met Ser Leu Val Lys Leu Gln Leu Cys His Met Leu Val
150           35           40           45
153 Glu Pro Asn Leu Cys Arg Ser Val Leu Ile Ala Asn Thr Val Arg Gln
154           50           55           60
157 Ile Gln Glu Glu Met Ser Gln Asp Gly Val Trp His Gly Met Ala Pro
158 65           70           75           80
161 Gln Asn Val Asp Arg Ala Pro Val Glu Arg Leu Val Ser Thr Glu Ile
162           85           90           95
165 Leu Cys Arg Thr Val Arg Gly Ala Glu Glu Glu His Pro Ala Pro Glu
166           100          105          110
169 Leu Glu Asp Ala Pro Leu Gln Asn Ser Val Ser Glu Leu Pro Ile Val
170           115          120          125
173 Gly Ser Ala Pro Gly Gln Arg Asn Pro Gln Ser Ser Leu Trp Glu Met
174           130          135          140
177 Asp Ser Pro Gln Glu Asn Arg Gly Ser Phe Gln Lys Ser Leu Asp Gln
178 145          150          155          160
181 Ile Phe Glu Thr Leu Glu Asn Lys Asn Ser Ser Ser Val Glu Glu Leu
182           165          170          175
185 Phe Ser Asp Val Asp Ser Ser Tyr Tyr Asp Leu Asp Thr Val Leu Thr
186           180          185          190
189 Gly Met Met Ser Gly Thr Lys Ser Ser Leu Cys Asn Gly Leu Glu Gly
190           195          200          205
193 Phe Ala Ala Ala Thr Pro Pro Pro Ser Ser Thr Cys Lys Ser Asp Leu
194           210          215          220
197 Ala Glu Leu Asp His Val Val Glu Ile Leu Val Glu Thr
198 225          230          235
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202 <211> LENGTH: 2082
203 <212> TYPE: DNA
204 <213> ORGANISM: Homo sapiens
206 <220> FEATURE:
207 <221> NAME/KEY: CDS
208 <222> LOCATION: (75)..(797)
210 <400> SEQUENCE: 3
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213 cgggtcagga caca atg ttt gca cga gga ctg aag agg aaa tgt gtt ggc      110
214           Met Phe Ala Arg Gly Leu Lys Arg Lys Cys Val Gly
215           1           5           10
217 cac gag gaa gac gtg gag gga gcc ctg gcc ggc ttg aag aca gtg tcc      158
218 His Glu Glu Asp Val Glu Gly Ala Leu Ala Gly Leu Lys Thr Val Ser
219           15           20           25
221 tca tac agc ctg cag cgg cag tcg ctc ctg gac atg tct ctg gtg aag      206
222 Ser Tyr Ser Leu Gln Arg Gln Ser Leu Leu Asp Met Ser Leu Val Lys
223           30           35           40
225 ttg cag ctt tgc cac atg ctt gtg gag ccc aac ctg tgc cgc tca gtc      254
226 Leu Gln Leu Cys His Met Leu Val Glu Pro Asn Leu Cys Arg Ser Val

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227 45          50          55          60
229 ctc att gcc aac acg gtc cgg cag atc caa gag gag atg acg cag gat      302
230 Leu Ile Ala Asn Thr Val Arg Gln Ile Gln Glu Glu Met Thr Gln Asp
231          65          70          75
233 ggg acg tgg cgc aca gtg gca ccc cag gct gca gag cgg gcg ccg ctc      350
234 Gly Thr Trp Arg Thr Val Ala Pro Gln Ala Ala Glu Arg Ala Pro Leu
235          80          85          90
237 gac cgc ttg gtc tcc acg gag atc ctg tgc cgt gca gcg tgg ggg caa      398
238 Asp Arg Leu Val Ser Thr Glu Ile Leu Cys Arg Ala Ala Trp Gly Gln
239          95          100          105
241 gag ggg gca cat cct gct cct ggc ttg ggg gac ggc cac aca cag ggt      446
242 Glu Gly Ala His Pro Ala Pro Gly Leu Gly Asp Gly His Thr Gln Gly
243          110          115          120
245 cca gtt tct gac ctt tgc cca gtc acc tca gca cag gca cca agg cac      494
246 Pro Val Ser Asp Leu Cys Pro Val Thr Ser Ala Gln Ala Pro Arg His
247 125          130          135          140
249 ctg cag agc agc gcc tgg gag atg gat ggc cct cga gaa aac aga gga      542
250 Leu Gln Ser Ser Ala Trp Glu Met Asp Gly Pro Arg Glu Asn Arg Gly
251          145          150          155
253 agc ttt cac aag tca ctt gat cag ata ttt gaa acg ctg gag act aaa      590
254 Ser Phe His Lys Ser Leu Asp Gln Ile Phe Glu Thr Leu Glu Thr Lys
255          160          165          170
257 aac ccc agc tgc atg gaa gag ctg ttc tca gac gtg gac agc ccc tac      638
258 Asn Pro Ser Cys Met Glu Glu Leu Phe Ser Asp Val Asp Ser Pro Tyr
259          175          180          185
261 tac gac ctg gac aca gta ctg aca ggc atg atg ggg ggt gcc agg ccg      686
262 Tyr Asp Leu Asp Thr Val Leu Thr Gly Met Met Gly Gly Ala Arg Pro
263          190          195          200
265 ggc ccc tgc gaa ggg ctc gag ggc ttg gct ccg gcc acc cca ggc cct      734
266 Gly Pro Cys Glu Gly Leu Glu Gly Leu Ala Pro Ala Thr Pro Gly Pro
267 205          210          215          220
269 agc tcc agc tgc aag tcc gac ctg ggc gag ctg gac cac gtg gtg gag      782
270 Ser Ser Ser Cys Lys Ser Asp Leu Gly Glu Leu Asp His Val Val Glu
271          225          230          235
273 atc ctg gtg gag acc tgagcaggag ccctgagtgc tcacagccgc ctctgacgca      837
274 Ile Leu Val Glu Thr
275          240
277 ttgacacgtg agcactggct cccacggagg gtgcgcctgc cgcacagcggc ccagccttgc      897
279 tgcctgtct gctgattctg agaaatccca gaacagccca ttaccagtgg ggctgcagcc      957
281 ctaggcccggt cccactcacc tccccctgt ggagcgccag gcagaggctg ttctggaagg      1017
283 cttcttgtct tctgacgtcc ccacagccct gggccctctg tgtctctttg tgtccccac      1077
285 tgtagaggac ggtgagccgc agctgcatca acctcctttt acctttagat aggtgaattt      1137
287 ttacaattca gttttacatg ttttgggcag tattttgtct taagatatat tttttaaact      1197
289 ttttatacct tatctcttta gattttttca gctattttct taaaagtata tttttctat      1257
291 aaacatcctt tgctgctaca ttagaacttt tatagcctaa acaattgcag ttggtgtgtt      1317
293 tcattttttt aagggtttaa taagggtttt ttgttttgtt ttgttttttg cagtgcagcat      1377
295 cactacagtc tcagtcacaa gtgtgaatgt atcatgtttt actttaaatg tgtgtgtgat      1437
297 acttcttcct tatgtctctg gctgcagtga gacctgggtg aaaatcagga gccgcacaca      1497
299 gccacatctt cctagacctt agagtaaatt atggaggatt ttatttatgt ctatttatat      1557

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301 gtaaagtgtca ttgaagacaa aggtcaaata tttgtctgtt tgtagatcac aggcaccagt 1617
303 tgggtcttcag ggacctcata gcccctcggg ggtgccttct caaggcagtg ttcctggagg 1677
305 ctcccatcag ggtcagccca tgcacctgcc ctgggtgagg aagtagcatt gctgctggat 1737
307 gagaaacgcc tgcgctgctc tgttagactg gtgctgaaac aaaagggtta ggctagggtg 1797
309 aagtctagaa tgaaagaaat ctgaatccat gtcattcata accccttgat ctgtagtgtc 1857
311 atgggtgctg ccgcaggcag ggagtgaagt ggggggtgct gcagccttcc actcctgccc 1917
313 cgctcacccc cacatgctcc ctgtttctca tgtttctct aacttctca ccccttaacc 1977
315 aaaaagggtgt gttttctttt gtgcataatag ccattcttaa atatcagtga tgtaaacctc 2037
317 actttatttaa aaaattatcc agcaaaaaaa aaaaaaaaaa aaaaaa 2082

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320 <210> SEQ ID NO: 4

321 <211> LENGTH: 241

322 <212> TYPE: PRT

323 <213> ORGANISM: Homo sapiens

325 <400> SEQUENCE: 4

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327 Met Phe Ala Arg Gly Leu Lys Arg Lys Cys Val Gly His Glu Glu Asp
328 1 5 10 15
331 Val Glu Gly Ala Leu Ala Gly Leu Lys Thr Val Ser Ser Tyr Ser Leu
332 20 25 30
335 Gln Arg Gln Ser Leu Leu Asp Met Ser Leu Val Lys Leu Gln Leu Cys
336 35 40 45
339 His Met Leu Val Glu Pro Asn Leu Cys Arg Ser Val Leu Ile Ala Asn
340 50 55 60
343 Thr Val Arg Gln Ile Gln Glu Glu Met Thr Gln Asp Gly Thr Trp Arg
344 65 70 75 80
347 Thr Val Ala Pro Gln Ala Ala Glu Arg Ala Pro Leu Asp Arg Leu Val
348 85 90 95
351 Ser Thr Glu Ile Leu Cys Arg Ala Ala Trp Gly Gln Glu Gly Ala His
352 100 105 110
355 Pro Ala Pro Gly Leu Gly Asp Gly His Thr Gln Gly Pro Val Ser Asp
356 115 120 125
359 Leu Cys Pro Val Thr Ser Ala Gln Ala Pro Arg His Leu Gln Ser Ser
360 130 135 140
363 Ala Trp Glu Met Asp Gly Pro Arg Glu Asn Arg Gly Ser Phe His Lys
364 145 150 155 160
367 Ser Leu Asp Gln Ile Phe Glu Thr Leu Glu Thr Lys Asn Pro Ser Cys
368 165 170 175
371 Met Glu Glu Leu Phe Ser Asp Val Asp Ser Pro Tyr Tyr Asp Leu Asp
372 180 185 190
375 Thr Val Leu Thr Gly Met Met Gly Gly Ala Arg Pro Gly Pro Cys Glu
376 195 200 205
379 Gly Leu Glu Gly Leu Ala Pro Ala Thr Pro Gly Pro Ser Ser Ser Cys
380 210 215 220
383 Lys Ser Asp Leu Gly Glu Leu Asp His Val Val Glu Ile Leu Val Glu
384 225 230 235 240
387 Thr

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391 <210> SEQ ID NO: 5

392 <211> LENGTH: 106

393 <212> TYPE: PRT

394 <213> ORGANISM: Danio rerio

VERIFICATION SUMMARY

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Input Set : A:\hepp sequence listing-US.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date.